RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY SYSTEMS BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/445,174_

Source: _1655_

Date Processed by STIC: _7-26-00_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,

2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u> <u>SUGGESTED CORRECTION</u>   SERIAL NUMBER: _O 9/445, 174_

RECEIVED

AUG 16 2000

TECH CENTER 1600/2900

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>**
sections for Artificial or Unknown sequences.

8 _____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 ✓ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature (NEW RULES)
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

AKS-Biotechnology Systems Branch- 5/15/99

1655

```
RAW SEQUENCE LISTING                    DATE: 07/26/2000
PATENT APPLICATION:  US/09/445,174      TIME: 10:17:06

         Input Set : A:\115541_1.txt
         Output Set: N:\CRF3\07262000\I445174.raw
```

```
 1 <110> APPLICANT: van Ommen, Garrit J.B.
 2         Petrij-Bosch, Anne
 3         Bakker, Egbert
 4         Devilee, Peter
 7 <120> TITLE OF INVENTION: A diagnostic test kit for determining a predisposition
 8         for breast and ovarian cancer, materials and methods
 9         for such determination
11 <130> FILE REFERENCE: P22163CA00
13 <140> CURRENT APPLICATION NUMBER: US 09/445,174
14 <141> CURRENT FILING DATE: 2000-04-24
16 <150> PRIOR APPLICATION NUMBER: PCT/NL98/00325
17 <151> PRIOR FILING DATE: 1998-06-03
19 <150> PRIOR APPLICATION NUMBER: EP 97201700.8
20 <151> PRIOR FILING DATE: 1997-06-04
22 <160> NUMBER OF SEQ ID NOS: 23
24 <170> SOFTWARE: PatentIn Ver. 2.1
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 20
28 <212> TYPE: DNA
29 <213> ORGANISM: Artificial Sequence
31 <220> FEATURE:
32 <223> OTHER INFORMATION: Description of Artificial Sequence: primer forward
33         for D17S1322
35 <400> SEQUENCE: 1
36 ctagcctggg caacaaacga                              20
39 <210> SEQ ID NO: 2
40 <211> LENGTH: 20
41 <212> TYPE: DNA
42 <213> ORGANISM: Artificial Sequence
44 <220> FEATURE:
45 <223> OTHER INFORMATION: Description of Artificial Sequence: primer reverse
46         for D17S1322
48 <400> SEQUENCE: 2
49 gcaggaagca ggaatggaac                              20
52 <210> SEQ ID NO: 3
53 <211> LENGTH: 21
54 <212> TYPE: DNA
55 <213> ORGANISM: Artificial Sequence
57 <220> FEATURE:
58 <223> OTHER INFORMATION: Description of Artificial Sequence: primer forward
59         for D17S855
61 <400> SEQUENCE: 3
62 ggatggcctt ttagaaagtg g                            21
65 <210> SEQ ID NO: 4
66 <211> LENGTH: 20
67 <212> TYPE: DNA
68 <213> ORGANISM: Artificial Sequence
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```
 70 <220> FEATURE:
 71 <223> OTHER INFORMATION: Description of Artificial Sequence: primer reverse
 72       for D17S855
 74 <400> SEQUENCE: 4
 75 acacagactt gtcctactgc                                              20
 78 <210> SEQ ID NO: 5
 79 <211> LENGTH: 20
 80 <212> TYPE: DNA
 81 <213> ORGANISM: Artificial Sequence
 83 <220> FEATURE:
 84 <223> OTHER INFORMATION: Description of Artificial Sequence: primer forward
 85       for D17S1323
 87 <400> SEQUENCE: 5
 88 taggagatgg attattggtg                                              20
 91 <210> SEQ ID NO: 6
 92 <211> LENGTH: 20
 93 <212> TYPE: DNA
 94 <213> ORGANISM: Artificial Sequence
 96 <220> FEATURE:
 97 <223> OTHER INFORMATION: Description of Artificial Sequence: primer reverse
 98       for D17S1323
100 <400> SEQUENCE: 6
101 aagcaacttt gcaatgagtg                                              20
104 <210> SEQ ID NO: 7
105 <211> LENGTH: 22
106 <212> TYPE: DNA
107 <213> ORGANISM: Artificial Sequence
109 <220> FEATURE:
110 <223> OTHER INFORMATION: Description of Artificial Sequence: primer forward
111       for first PCR
113 <400> SEQUENCE: 7
114 tcacagtgca gtgaattgga ag                                           22
117 <210> SEQ ID NO: 8
118 <211> LENGTH: 24
119 <212> TYPE: DNA
120 <213> ORGANISM: Artificial Sequence
122 <220> FEATURE:
123 <223> OTHER INFORMATION: Description of Artificial Sequence: primer reverse
124       for first PCR
126 <400> SEQUENCE: 8
127 gtagccagga cagtagaagg actg                                         24
130 <210> SEQ ID NO: 9
131 <211> LENGTH: 22
132 <212> TYPE: DNA
133 <213> ORGANISM: Artificial Sequence
135 <220> FEATURE:
136 <223> OTHER INFORMATION: Description of Artificial Sequence: primer forward
137       for second PCR
139 <400> SEQUENCE: 9
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140 gaagaaagag gaacgggctt gg                                       22
143 <210> SEQ ID NO: 10
144 <211> LENGTH: 21
145 <212> TYPE: DNA
146 <213> ORGANISM: Artificial Sequence
148 <220> FEATURE:
149 <223> OTHER INFORMATION: Description of Artificial Sequence: primer reverse
150       for second PCR
152 <400> SEQUENCE: 10
153 ggccactttg taagctcatt c                                        21
156 <210> SEQ ID NO: 11
157 <211> LENGTH: 19
158 <212> TYPE: DNA
159 <213> ORGANISM: Artificial Sequence
161 <220> FEATURE:
162 <223> OTHER INFORMATION: Description of Artificial Sequence: primer forward
164 <400> SEQUENCE: 11
165 aaccaccaag gtccaaagc                                           19
168 <210> SEQ ID NO: 12
169 <211> LENGTH: 24
170 <212> TYPE: DNA
171 <213> ORGANISM: Artificial Sequence
173 <220> FEATURE:
174 <223> OTHER INFORMATION: Description of Artificial Sequence: primer reverse
176 <400> SEQUENCE: 12
177 gtagccagga cagtagaagg actg                                     24
180 <210> SEQ ID NO: 13
181 <211> LENGTH: 20
182 <212> TYPE: DNA
183 <213> ORGANISM: Artificial Sequence
185 <220> FEATURE:
186 <223> OTHER INFORMATION: Description of Artificial Sequence: primer reverse
188 <400> SEQUENCE: 13
189 tacgtgggtt caactgaagc                                          20
192 <210> SEQ ID NO: 14
193 <211> LENGTH: 20
194 <212> TYPE: DNA
195 <213> ORGANISM: Artificial Sequence
197 <220> FEATURE:
198 <223> OTHER INFORMATION: Description of Artificial Sequence: primer forward
200 <400> SEQUENCE: 14
201 tcccattgag aggtcttgct                                          20
204 <210> SEQ ID NO: 15
205 <211> LENGTH: 20
206 <212> TYPE: DNA
207 <213> ORGANISM: Artificial Sequence
209 <220> FEATURE:
210 <223> OTHER INFORMATION: Description of Artificial Sequence: primer reverse
212 <400> SEQUENCE: 15
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213 actgtgctac tcaagcacca                                    20
216 <210> SEQ ID NO: 16
217 <211> LENGTH: 24
218 <212> TYPE: DNA
219 <213> ORGANISM: Artificial Sequence
221 <220> FEATURE:
222 <223> OTHER INFORMATION: Description of Artificial Sequence: primer forward
224 <400> SEQUENCE: 16
225 gaaaaaaaag tacaaccaaa tgcc                                24
228 <210> SEQ ID NO: 17
229 <211> LENGTH: 24
230 <212> TYPE: DNA
231 <213> ORGANISM: Artificial Sequence
233 <220> FEATURE:
234 <223> OTHER INFORMATION: Description of Artificial Sequence: primer reverse
236 <400> SEQUENCE: 17
237 agcccacttc attagtactg gaac                                24
240 <210> SEQ ID NO: 18
241 <211> LENGTH: 24
242 <212> TYPE: DNA
243 <213> ORGANISM: Artificial Sequence
245 <220> FEATURE:
246 <223> OTHER INFORMATION: Description of Artificial Sequence: primer forward
248 <400> SEQUENCE: 18
249 taccctataa gccagaatcc agaa                                24
252 <210> SEQ ID NO: 19
253 <211> LENGTH: 21
254 <212> TYPE: DNA
255 <213> ORGANISM: Artificial Sequence
257 <220> FEATURE:
258 <223> OTHER INFORMATION: Description of Artificial Sequence: primer reverse
260 <400> SEQUENCE: 19
261 ggccactttg taagctcatt c                                   21
264 <210> SEQ ID NO: 20
265 <211> LENGTH: 720
266 <212> TYPE: DNA
267 <213> ORGANISM: Homo sapiens
269 <220> FEATURE:
270 <223> OTHER INFORMATION: /note="Exon 22 of BRCA1 and its flanking intron
271        sequences, pos. 79441-80160"
273 <400> SEQUENCE: 20
274 agaggtcttg ctataagcct tcatccggag agtgtagggt agagggcctg ggttaagtat 60
275 gcagattact gcagtgattt tacatctaaa tgtccatttt agatcaactg gaatggatgg 120
276 tacagctgtg tggtgcttct gtggtgaagg agctttcatc attcaccctt ggcacagtaa 180
277 gtattgggtg ccctgtcaga gagggaggac acaatattct ctcctgtgag caagactggc 240
278 acctgtcagt ccctatggat gcccctactg tagcctcaga agtcttctct gcccacatac 300
279 ctgtgccaaa agactccatc tgtaagggat gggtaaggat ttgagaactg cacatattaa 360
280 atatactgag ggaagacttt ttccctctaa ctctttttcc catatgtccc tcccctcct 420
281 ctctgtgact gccccagcat actgtgtttc aacaaatcat caagaaatga tgggctggag 480
```

RAW SEQUENCE LISTING   DATE: 07/26/2000
PATENT APPLICATION: US/09/445,174   TIME: 10:17:06

```
        Input Set : A:\115541_1.txt
        Output Set: N:\CRF3\07262000\I445174.raw

    282 gctgggcatg gtggctcatg tctgtaatcc cagcactttg ggaggccgag gcaggtggat 540
    283 cacttgtcag gagtttgaga ccagcctggc caacatggtg aaaccccatc tgtactaaaa 600
    284 aaaaaaaaac aaaaagtagc caggcctggt ggagcatgcc tgtaatgcca gctatttggg 660
    285 aagttgaggt gtgagcatcg cttgaacgtg ggaggcagag gttgcagtga gccaagattg 720
    288 <210> SEQ ID NO: 21
    289 <211> LENGTH: 180
    290 <212> TYPE: DNA
    291 <213> ORGANISM: Homo sapiens
    293 <220> FEATURE:
    294 <223> OTHER INFORMATION: /note="Intronic region flanking exon 12, pos.
    295       44423 - 44600"
    297 <400> SEQUENCE: 21
W--> 298 cctgtaatcc cagcactttg ggaggccgag gcgggaggat catgtgnngt caggagatcc 60
    299 agaccatcct ggctaacacg gtgaaacacc atttctacta aaactacaaa aaattagctg 120
    300 ggcatggtgg cgggcgcctg taatcccagc tactcaggag gctgaagcag aagaatggct 180
    303 <210> SEQ ID NO: 22
    304 <211> LENGTH: 180
    305 <212> TYPE: DNA
    306 <213> ORGANISM: Homo sapiens
    308 <220> FEATURE:
    309 <223> OTHER INFORMATION: /note="Intronic region flanking exon 13, pos.
    310       48256 - 48436"
    312 <400> SEQUENCE: 22
    313 cctgtaaccc cagcactttg ggaggccaag gcaggcgaat cacctgaggt cgggagctcg 60
    314 agaccagcct gaccaacatg gagaaaccac atctctacta aaactacaaa aaattagccg 120
    315 ggcgtggtgg cacatgcctg taatcccagc tacttgggag ctacggtgcc tggcctagtt 180
    318 <210> SEQ ID NO: 23
    319 <211> LENGTH: 60
    320 <212> TYPE: DNA
    321 <213> ORGANISM: Homo sapiens
    323 <220> FEATURE:
    324 <223> OTHER INFORMATION: /note="Deletion-function fragment"
    326 <400> SEQUENCE: 23
    327 agaccatcct ggctaacacg gtgaaacacc atttctacta aaactacaaa aaattagccg 60
```

(handwritten annotations in right margin:) Mandatory features missing <221> <222> <223> of. Explain location of n's and residues they represent. See #10 on Error Summary Sheet.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/445,174

DATE: 07/26/2000
TIME: 10:17:07

Input Set : A:\115541_1.txt
Output Set: N:\CRF3\07262000\I445174.raw

L:298 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:21
L:298 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:21
L:298 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:21